STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

**The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:**

Application Serial Number: _09/900, 963 B_

Source: _JFW16,_

Date Processed by STIC: _12/15/2005_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
    APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
    NOTICE TO COMPLY**
**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER
VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
    User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
    U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
    Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/900, 963B_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

~~Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.~~
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:31

     Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
     Output Set: N:\CRF4\12152005\I900963B.raw

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    1 <110> APPLICANT: GUERIN-MARCHAND, CLAUDINE
    2        DRUILHE, PIERRE
    3 <120> TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P.
FALCIPARUM
    4        BEARING EPITOPES CAPABLE OF STIMULATING THE T LYMPHOCYTES
    5 <130> FILE REFERENCE: 010830-118
C-->  6 <140> CURRENT APPLICATION NUMBER: US/09/900,963B
    7 <141> CURRENT FILING DATE: 2001-07-10
    8 <150> PRIOR APPLICATION NUMBER: 08/098,327
    9 <151> PRIOR FILING DATE: 1993-11-24
   10 <150> PRIOR APPLICATION NUMBER: PCT/FR92/00104
   11 <151> PRIOR FILING DATE: 1992-02-05
   12 <150> PRIOR APPLICATION NUMBER: FR 91 01286
   13 <151> PRIOR FILING DATE: 1991-02-05
   14 <160> NUMBER OF SEQ ID NOS: 47
   15 <170> SOFTWARE: PatentIn Ver. 3.3
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pp 1-2, 5, 7

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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  769 <211> LENGTH: 954
  770 <212> TYPE: DNA
  771 <213> ORGANISM: Plasmodium falciparum
  772 <221> NAME/KEY: CDS
  773 <222> LOCATION: (1)..(954)
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  775        atg aaa cat att ttg tac ata tca ttt tac ttt atc ctt gtt aat tta      48
  776        Met Lys His Ile Leu Tyr Ile Ser Phe Tyr Phe Ile Leu Val Asn Leu
  777         1               5                   10                  15
  778        ttg ata ttt cat ata aat gga aag ata ata aag aat tct gaa aaa gat      96
  779        Leu Ile Phe His Ile Asn Gly Lys Ile Ile Lys Asn Ser Glu Lys Asp
  780                       20                  25                  30
  781        gaa atc ata aaa tct aac ttg aga agt ggt tct tca aat tct agg aat     144
  782        Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn
  783                     35                  40                  45
  784        cga ata aat gag gaa aat cac gag aag aaa cac gtt tta tct cat aat     192
  785        Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn
  786              50                  55                  60
  787        tca tat gag aaa act aaa aat aat gaa aat aat aaa ttt ttc gat aag     240
  788        Ser Tyr Glu Lys Thr Lys Asn Asn Glu Asn Asn Lys Phe Phe Asp Lys
  789           65                  70                  75                  80
  790        gat aaa gag tta acg atg tct aat gta aaa aat gtg tca caa aca aat     288
  791        Asp Lys Glu Leu Thr Met Ser Asn Val Lys Asn Val Ser Gln Thr Asn
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Insert ＜220＞ whenever ＜221＞, ＜222＞ or ＜223＞ is shown ＜220＞ never has a response it is a header only.

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792                        85              90              95
793     ttc aaa agt ctt tta aga aat ctt ggt gtt tca gag aat ata ttc ctt    336
794     Phe Lys Ser Leu Leu Arg Asn Leu Gly Val Ser Glu Asn Ile Phe Leu
795                   100             105             110
796     aaa gaa aat aaa tta aat aag gaa ggg aaa tta att gaa cac ata ata    384
797     Lys Glu Asn Lys Leu Asn Lys Glu Gly Lys Leu Ile Glu His Ile Ile
798               115             120             125
799     aat gat gat gac gat aaa aaa aaa tat att aaa ggg caa gac gaa aac    432
800     Asn Asp Asp Asp Asp Lys Lys Lys Tyr Ile Lys Gly Gln Asp Glu Asn
801           130             135             140
802     aga caa gaa gat ctt gaa gaa aaa gca gct aaa gaa aag tta cag ggg    480
803     Arg Gln Glu Asp Leu Glu Glu Lys Ala Ala Lys Glu Lys Leu Gln Gly
804     145             150             155             160
805     caa caa agc gat tca gaa caa gag aga cgt gct aaa gaa aag ttg caa    528
806     Gln Gln Ser Asp Ser Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln
807                   165             170             175
808     gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa aag ttg    576
809     Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu Lys Leu
810                   180             185             190
811     caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa gaa aag    624
812     Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys
813               195             200             205
814     ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa    672
815     Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu
816           210             215             220
817     aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa    720
818     Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys
819     225             230             235             240
820     gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt gct    768
821     Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
822                   245             250             255
823     aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt    816
824     Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu
825                   260             265             270
826     gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gat aga    864
827     Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
828               275             280             285
829     ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag    912
830     Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
831           290             295             300
832     aga cgt gct aaa gaa agg ttg caa gaa caa caa agc gat tta          954
833     Arg Arg Ala Lys Glu Arg Leu Gln Glu Gln Gln Ser Asp Leu
834     305             310             315
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<212> TYPE: DNA
<213> ORGANISM: Plasmodium falciparum
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Insert > <220>

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     936      1               5                   10                  15
     937     ttg caa gaa caa caa agc gat tta gaa caa gat aga ctt gct aaa gaa    96
     938     Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
     939                  20                  25                  30
     940     aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
     941     Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
     942              35                  40                  45
     943     gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
     944     Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
     945          50                  55                  60
     946     aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
     947     Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
     948      65                  70                  75                  80
     949     gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
     950     Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
     951                  85                  90                  95
     952     ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
     953     Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
     954              100                 105                 110
     955     aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
     956     Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
     957              115                 120                 125
     958     gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
     959     Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
     960          130                 135                 140
     961     caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
     962     Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
     963     145                 150                 155                 160
     964     gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
     965     Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
     966              165                 170                 175
     967     tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
     968     Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
     969              180                 185                 190
     970     gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
     971     Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
     972              195                 200                 205
     973     aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
     974     Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
     975     210                 215                 220
     976     aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
     977     Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
     978     225                 230                 235                 240
     979     gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat   768
     980     Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
     981              245                 250                 255
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982        ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga    816
983        Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
984                    260                 265                 270
985        gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att    864
986        Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
987                    275                 280                 285
988        aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa    912
989        Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
990            290                 295                 300
991        gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct    960
992        Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
993        305                 310                 315                 320
994        gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt    1008
995        Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
996                    325                 330                 335
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998        Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr
999                    340                 345                 350
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1001       Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu
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1008       385                 390                 395                 400
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1010       Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
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1012       gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat    1296
1013       Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1014                   420                 425                 430
1015       ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat    1344
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1017                   435                 440                 445
1018       aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca    1392
1019       Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser
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1022       Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp
1023       465                 470                 475                 480
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E--> 1117	<400> SEQUENCE: 46			

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1122      Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
1123                      20                  25                  30
1124      aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
1125      Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
1126                  35                  40                  45
1127      gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
1128      Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
1129                  50                  55                  60
1130      aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
1131      Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
1132       65                  70                  75                  80
1133      gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
1134      Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
1135                      85                  90                  95
1136      ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
1137      Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
1138                  100                 105                 110
1139      aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
1140      Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
1141                  115                 120                 125
1142      gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
1143      Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
1144                  130                 135                 140
1145      caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
1146      Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
1147      145                 150                 155                 160
1148      gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
1149      Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
1150                  165                 170                 175
1151      tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
1152      Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
1153                  180                 185                 190
1154      gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
1155      Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
1156                  195                 200                 205
1157      aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
1158      Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
1159                  210                 215                 220
1160      aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
1161      Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
1162      225                 230                 235                 240
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1163	gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat	768
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1165	245 250 255	
1166	ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga	816
1167	Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg	
1168	260 265 270	
1169	gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att	864
1170	Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile	
1171	275 280 285	
1172	aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa	912
1173	Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu	
1174	290 295 300	
1175	gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct	960
1176	Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser	
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1178	gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt	1008
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1182	Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr	
1183	340 345 350	
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1185	Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu	
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1187	ttt aag cct att gtg caa tat gac aat ttc caa gat gaa gaa aac ata	1152
1188	Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile	
1189	370 375 380	
1190	gga att tat aaa gaa cta gaa gat ttg ata gag aaa aat gaa aat tta	1200
1191	Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu	
1192	385 390 395 400	
1193	gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa	1248
1194	Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu	
1195	405 410 415	
1196	gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat	1296
1197	Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn	
1198	420 425 430	
1199	ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat	1344
1200	Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr	
1201	435 440 445	
1202	aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca	1392
1203	Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser	
1204	450 455 460	
1205	ttg ttt cat ata ttt gac gga gac aat gaa att tta cag atc gtg gat	1440
1206	Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp	
1207	465 470 475 480	
1208	gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt	1488
1209	Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu	
1210	485 490	
1211	ata tat	1494

<210> 1
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Formula Sequence

<220>
<221> VARIANT
<222> 8
<223> Xaa = Glu or Gly

<400> 1
Leu Ala Lys Glu Lys Leu Gln Xaa Gln Gln Ser Asp Leu Glu Gln Glu
 1   5   10   15
Arg

Insufficient Explanation. Give Source(s) of genetic material (See item 11 on Error Summary Sheet).

The above is a Sample of Global Error

PY1

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/15/2005
PATENT APPLICATION: **US/09/900,963B**   TIME: 08:47:32

Input Set : **N:\Crf4\Refhold\09_folder\I900963B.raw**
Output Set: **N:\CRF4\12152005\I900963B.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY　　　　　　　　DATE: 12/15/2005
PATENT APPLICATION:　**US/09/900,963B**　　　TIME: 08:47:32

Input Set : **N:\Crf4\Refhold\09_folder\I900963B.raw**
Output Set: **N:\CRF4\12152005\I900963B.raw**

```
L:6 M:270 C: Current Application Number differs, Wrong Format
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:38 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:774 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:933 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:1117 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46
```